

Preface

This volume comprises the formal proceedings of the Fourth International Conference on Intelligent Systems for Molecular Biology (ISMB-96) held at Washington University in St. Louis from June 12 to June 15, 1996. The previous ISMB meetings successfully brought together computer scientists and molecular biologists from many countries, and it is the aim of the fourth ISMB conference to be as successful.

A special emphasis at ISMB-96 was genome analysis, as this year marks the completion of the sequencing of several genomes, including an eubacteria (*H. influenza*) and an eukaryote (*S. cerevisiae*), and the beginning of large scale human genome sequencing. Computational science has played a fundamental role in the progress of the Human Genome Project. Major contributions include the formulation of fingerprint mapping strategies, computationally efficient algorithms for physical and genetic map assembly, automated lane-tracking, basecalling, and sequence assembly, automated gene recognition, and efficient algorithms for sequence similarity identification. Databases and network information retrieval tools have been essential in coordinating a globally distributed project and in disseminating the results to biologists worldwide. It is no exaggeration to say that the Human Genome Project could not have achieved its success without the active involvement of computational scientists. The integration of structural biology, biophysics, and molecular sequence analysis in many papers has been particularly gratifying.

The high level of interest in the ISMB conferences has been maintained. A distinguished program committee that included both computational scientists and experimental biologists from leading institutions around the world was assembled. The committee has grown to 44 members, including several new members from the genome mapping and sequencing community. The call for papers produced 65 submissions that were of high standard that reflected the international character of the conference, with submissions received from the North America, Europe, Asia, and Australia. All papers were rigorously reviewed by at least three members of the program committee, and the program for the conference was assembled based on their recom-

mendations. Only those papers that could be presented as full talks at the conference were accepted for publication as full papers in the proceedings. Thus, we were more selective in accepting papers this year and only 27 top-quality papers were included in these proceedings. All attendees at the conference were encouraged to present at the open poster sessions. The poster abstracts were made available as World Web Web documents, and were published in a separate booklet.

There are an increasing number of versatile and useful software tools in computational biology for gene identification, sequence similarity detection, pattern/motif identification, structure prediction, and other important problems. These tools bridge the gap between theory and practice. An oral presentation is often not enough to provide the audience with a true feeling for the tool's utility. Therefore, we have added special sessions that will enable presenters to provide an interactive demonstration using the World Wide Web.

Keynote addresses were given by four eminent speakers: Professor Russell Doolittle from the University of California at San Diego, Professor David Haussler from the University of California at Santa Cruz, Professor Chris Sander from the EMBL-EBI at Cambridge, and Professor Robert Waterston from Washington University.

Once again, ISMB was able to offer participants a selection of diverse and high-quality tutorial presentations. From a total of 20 proposals, 8 were selected at both introductory and advanced levels and presented by experienced instructors, including several drawn from the program committee.

As a service to the community, ISMB introduced a job fair this year, giving computational biologists an opportunity to meet with prospective employers. By offering services such as a published proceedings, a job fair, and the meeting itself, we hope to catalyze the formation of an academic society for computational biologists.

To make the conference accessible to younger scientists and trainees, the organizing committee successfully applied for and received both federal and private funding. The Organizing Committee would especially like to thank the National Institutes for Health and the Department of Energy for grants, and

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